Pillotina corrugata sp. nov., Hollandina grandis sp. nov. and Hollandinoides gharagozlouae gen. nov. sp. nov.

Submitted by Treitli, Sebastian Cristian

Genus *Hollandinoides*

Etymology
[Ho.llan.di.no.i'des] **N.L. fem. n.** *Hollandina*, a genus of spirochetes; **L. neut. adj. suff.** *-oides*, resembling; **N.L. neut. n.** *Hollandinoides*, a *Hollandina*-like genus

Nomenclatural type
Species *Hollandinoides gharagozlouae*[Ts]

Description
Large helical cells that colonize the hindgut of the termite *Reticulitermes flavipes*. They can be detected with the 16S rRNA-targeted oligonucleotide probe Rf-HolD1-990 (5'-GGCTTCCCCACTATGTCAAA-3'). The type genome is from the hindgut of the termite *Reticulitermes flavipes*.

Classification
Bacteria » *Spirochaetota* » *Spirochaetia* » *Spirochaetales* » “Breznakiellaceae” » *Hollandinoides*

References
Effective publication: Treitli et al., 2026 [1]

Registry URL
https://seqco.de/i:54983

Species *Hollandina grandis*

Etymology
[gran'dis] **L. fem. adj.** *grandis*, large

Nomenclatural type
NCBI Assembly: GCA_054669045.1 [Ts]

Description
Helical cells are rounded to oblong in cross sections, with a diameter of 0.5–0.7µm at the widest point. The length varies between 30 and 80 µm. Approx. 70–80 periplasmic flagella. The rounded protoplasmic cylinder is 0.4–0.5 µm in diameter. Members of this species colonize the hindgut of the genus *Incisitermes*. They can be detected with the 16S rRNA-targeted oligonucleotide probe It-Hol-183 (5'-CCATGCCACAGCACGATAAG-3'). The type genome is from the hindgut of the termite *Incisitermes tabogae*.

Includes all genomes that show ≥95% average nucleotide identity (ANI) to the type genome. The type genome has an estimated size of 3.72 Mbp and a GC content of 49.1 mol%.

Classification
Bacteria » *Spirochaetota* » *Spirochaetia* » *Spirochaetales* » *Spirochaetaceae* » *Hollandina* » *Hollandina grandis*

References
Effective publication: Treitli et al., 2026 [1]

Registry URL
https://seqco.de/i:51495

Species *Hollandinoides gharagozlouae*[Ts]

Etymology
[gha.ra.goz.lou'ae] **N.L. gen. n.** *gharagozlouae*, of Gharagozlou, in honor of Iran Dokht Gharagozlou, an Iranian/French structural biologist

Nomenclatural type
NCBI Assembly: GCA_054965555.1 [Ts]

Description
Large helical cells that colonize the hindgut of the termite *Reticulitermes flavipes*. They can be detected with the 16S rRNA-targeted oligonucleotide probe Rf-HolD1-990 (5'-GGCTTCCCCACTATGTCAAA-3'). The type genome is from the hindgut of the termite *Reticulitermes flavipes*.

Classification
Bacteria » *Spirochaetota* » *Spirochaetia* » *Spirochaetales* » “Breznakiellaceae” » *Hollandinoides* » *Hollandinoides gharagozlouae*[Ts]

References
Effective publication: Treitli et al., 2026 [1]

Registry URL
https://seqco.de/i:54982

Species *Pillotina corrugata*

Etymology
[cor.ru.ga'ta] **L. fem. part. adj.** *corrugata*, wrinkled, corrugated

Nomenclatural type
NCBI Assembly: GCA_054669185.1 [Ts]

Description
Helical cells are 0.9–1.2 µm in diameter, with 26–30 parallel ridges. The length varies between 40 and 90 µm. Approx. 70–100 periplasmic flagella. The protoplasmic cylinder is 0.4–0.5 µm in diameter. Members of this species colonize the hindgut of the genus *Kalotermes*. They can be detected with the 16S rRNA-targeted oligonucleotide probe Kf-Pil-1449 (5'-GCAGCGCCCTCCTTTTACAA-3'). The type genome is from *Kalotermes flavicollis*.

Includes all genomes that show ≥95% average nucleotide identity (ANI) to the type genome. The type genome has an estimated genome size of 3.14 Mbp and a GC content of 43.2 mol%.

Classification
Bacteria » *Spirochaetota* » *Spirochaetia* » *Spirochaetales* » *Spirochaetaceae* » *Pillotina* » *Pillotina corrugata*

References
Effective publication: Treitli et al., 2026 [1]

Registry URL
https://seqco.de/i:51288

References

1. Treitli et al. (2026). Metabolic capacities of large “pillotinaceous” spirochetes from termite guts and their placement among Breznakiellaceae. *BMC Biology*. DOI:10.1186/s12915-026-02591-x

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:udhxf-g0** submitted by **Treitli, Sebastian Cristian** and including 4 new names has been successfully validated.

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